

SUBSTITUTE SEQUENCE LISTING

<110> Degussa AG

<120> Cyanide-tolerant nitrile hydratases

<130> 040061

<140> US/10/598,873

<141> 2006-09-14

<160> 14

<170> PatentIn version 3.3

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<223> Coding region of alpha-subunit gene

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<223> Coding region of beta-subunit gene

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<221> gene

<222> (1309)..(2577)

<223> Gene of activator protein

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ccg gtc gcg gag acg ttc gcc ttc ctt gac gct gat ggc ttc agc ctc Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asp Gly Phe Ser Leu 115 120 125			384
agc gaa ctg gcg cgc ctg gac acc ttg gtg acg gtg gtc gat ggc agt Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Gly Ser 130 135 140			432
cgt ttc cag gaa ctg ctc gaa tcg ccg cac acc gtt gac cag gat gac Arg Phe Gln Glu Leu Leu Glu Ser Pro His Thr Val Asp Gln Asp Asp 145 150 155 160			480
gcc acg cca gac gca ccc aag cgc cac ctg gcc gat ctg ctg atc gaa Ala Thr Pro Asp Ala Pro Lys Arg His Leu Ala Asp Leu Leu Ile Glu 165 170 175			528
cag gtg gag tac gcc aac gtc att ctc gtc aat aag ctg gat ctg atc Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Leu Asp Leu Ile 180 185 190			576
gat gca gcg cag tat cag gcc gtg cag gcg atc ctc aca ggc ctt aac Asp Ala Ala Gln Tyr Gln Ala Val Gln Ala Ile Leu Thr Gly Leu Asn 195 200 205			624
ccg acg gcg cgg atc atg ccg atg gcc cac ggt aac atc cca tca gcc Pro Thr Ala Arg Ile Met Pro Met Ala His Gly Asn Ile Pro Ser Ala 210 215 220			672
agc ctg ctc ggc acc cat ctg ttt gat tta ccc agc ctc gcg gcg tcg Ser Leu Leu Gly Thr His Leu Phe Asp Leu Pro Ser Leu Ala Ala Ser 225 230 235 240			720
ccg ggc tgg atg cgg aaa atg gag gcg gca gac gcg ccg gcc tcc gag Pro Gly Trp Met Arg Lys Met Glu Ala Ala Asp Ala Pro Ala Ser Glu 245 250 255			768
tcg gac acc tat ggc gtg acg tcc tgg gtg tac cgt gag cgc gca cct Ser Asp Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Glu Arg Ala Pro 260 265 270			816
ttc cac ccg caa cgg ttg ctc gac ttt ctc cag cag ccc tgg tgc aac Phe His Pro Gln Arg Leu Leu Asp Phe Leu Gln Gln Pro Trp Cys Asn 275 280 285			864
ggg cgg ttg ctg cgc agc aaa ggt tac ttc tgg ctt gcc agc cgc cac Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His 290 295 300			912

ctg	gaa	acc	ggc	ctg	ctg	gtg	caa	agc	ggc	aag	cgg	ttc	cag	tgg	gac	960
Leu	Glu	Thr	Gly	Leu	Leu	Val	Gln	Ser	Gly	Lys	Arg	Phe	Gln	Trp	Asp	
305					310					315					320	
tat	gtc	ggg	cgc	tgg	tgg	aac	ttc	atc	gag	ccg	tcg	caa	tgg	ccc	cgg	1008
Tyr	Val	Gly	Arg	Trp	Trp	Asn	Phe	Ile	Glu	Pro	Ser	Gln	Trp	Pro	Arg	
				325					330					335		
gac	gaa	tac	cgg	ctg	cag	ggc	atc	agg	gcc	aaa	tgg	gac	agc	gtg	gtc	1056
Asp	Glu	Tyr	Arg	Leu	Gln	Gly	Ile	Arg	Ala	Lys	Trp	Asp	Ser	Val	Val	
			340					345					350			

ggc gac tgc cgg cag gag ttg gtg ttt atc ggc cag ggc ctc gac acc	1104
Gly Asp Cys Arg Gln Glu Leu Val Phe Ile Gly Gln Gly Leu Asp Thr	
355 360 365	
gac gcg tta cag cgc gag ctc gac cac tgc ctg ctg agc gcc cag gaa	1152
Asp Ala Leu Gln Arg Glu Leu Asp His Cys Leu Leu Ser Ala Gln Glu	
370 375 380	
atc gcc gcc ggc cca ctg gcc tgg caa gcg ctg cca ggg gcg acc gcc	1200
Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala	
385 390 395 400	
ttt gac cga cag acc ctt gcc cgc ccc cca cac agc cca tgg cga ttg	1248
Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu	
405 410 415	
ccc cca ttt gat ccg aga tag	1269
Pro Pro Phe Asp Pro Arg	
420	

<210> 5
 <211> 422
 <212> PRT
 <213> *Pseudomonas marginalis*

<400> 5

Met Thr Asp Gly Ala Gln Ala Ser Arg Leu Pro Val Thr Val Leu Ser	
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Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg	
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Asn Arg Glu Gly Leu Arg Val Ala Val Ile Val Asn Asp Met Ser Glu	
35 40 45	
Val Asn Ile Asp Ala Glu Glu Val Gln Arg Asp Val Ala Leu His Arg	
50 55 60	
Gly Arg Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr	
65 70 75 80	
Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Met Leu Ala Arg Gln Gln	
85 90 95	
Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met	
100 105 110	
Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asp Gly Phe Ser Leu	
115 120 125	

Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Gly Ser
130 135 140

Arg Phe Gln Glu Leu Leu Glu Ser Pro His Thr Val Asp Gln Asp Asp
145 150 155 160

Ala Thr Pro Asp Ala Pro Lys Arg His Leu Ala Asp Leu Leu Ile Glu
165 170 175

Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Leu Asp Leu Ile
180 185 190

Asp Ala Ala Gln Tyr Gln Ala Val Gln Ala Ile Leu Thr Gly Leu Asn
195 200 205

Pro Thr Ala Arg Ile Met Pro Met Ala His Gly Asn Ile Pro Ser Ala
210 215 220

Ser Leu Leu Gly Thr His Leu Phe Asp Leu Pro Ser Leu Ala Ala Ser
225 230 235 240

Pro Gly Trp Met Arg Lys Met Glu Ala Ala Asp Ala Pro Ala Ser Glu
245 250 255

Ser Asp Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Glu Arg Ala Pro
260 265 270

Phe His Pro Gln Arg Leu Leu Asp Phe Leu Gln Gln Pro Trp Cys Asn
275 280 285

Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
290 295 300

Leu Glu Thr Gly Leu Leu Val Gln Ser Gly Lys Arg Phe Gln Trp Asp
305 310 315 320

Tyr Val Gly Arg Trp Trp Asn Phe Ile Glu Pro Ser Gln Trp Pro Arg
325 330 335

Asp Glu Tyr Arg Leu Gln Gly Ile Arg Ala Lys Trp Asp Ser Val Val
340 345 350

Gly Asp Cys Arg Gln Glu Leu Val Phe Ile Gly Gln Gly Leu Asp Thr
355 360 365

Asp Ala Leu Gln Arg Glu Leu Asp His Cys Leu Leu Ser Ala Gln Glu
 370 375 380
 Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala
 385 390 395 400

Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu
 405 410 415

Pro Pro Phe Asp Pro Arg
 420

<210> 6
 <211> 2371
 <212> DNA
 <213> Pseudomonas putida

<220>
 <221> CDS
 <222> (1)..(582)
 <223> Coding region of alpha-subunit gene

<220>
 <221> CDS
 <222> (624)..(1286)
 <223> Coding region of beta-subunit gene

<220>
 <221> gene
 <222> (1283)..(2371)
 <223> Gene of activator protein

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 Met Thr Ala Thr Ser Thr Pro Gly Glu Arg Ala Arg Ala Leu Phe Ala
 1 5 10 15
 gtg ctc aag cgc aaa gac ctc atc ccc gag ggc tac atc gaa cag ctc 96
 Val Leu Lys Arg Lys Asp Leu Ile Pro Glu Gly Tyr Ile Glu Gln Leu
 20 25 30
 acc cag ctg atg gaa cac ggc tgg agc ccg gaa aac ggc gcg cgc atc 144
 Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg Ile
 35 40 45
 gtc gcc aag gcc tgg gtc gat ccg cag ttt cgc gag ctg ctg ctc aag 192
 Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Glu Leu Leu Leu Lys
 50 55 60
 gac ggt acg gcc gcc tgc gcc cag ttc ggc ttc acc ggc cca caa ggc 240
 Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Phe Thr Gly Pro Gln Gly
 65 70 75 80
 gaa tac atc gtc gcc ctg gaa gac acc ccg cag ttg aaa aac gtg atc 288
 Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Gln Leu Lys Asn Val Ile
 85 90 95
 gtc tgt agc ctg tgc tcc tgc acg aac tgg ccg gtg ctg ggc ctg cca 336

Val	Cys	Ser	Leu	Cys	Ser	Cys	Thr	Asn	Trp	Pro	Val	Leu	Gly	Leu	Pro		
			100					105					110				
cct	gag	tgg	tac	aag	ggc	ttc	gag	ttc	cgt	gcg	cgg	ttg	gtc	cgg	gag		384
Pro	Glu	Trp	Tyr	Lys	Gly	Phe	Glu	Phe	Arg	Ala	Arg	Leu	Val	Arg	Glu		
		115					120					125					
ggg	cgc	acg	gta	ttg	cgc	gag	ctg	ggc	acc	gag	ttg	ccc	ggc	gac	atg		432
Gly	Arg	Thr	Val	Leu	Arg	Glu	Leu	Gly	Thr	Glu	Leu	Pro	Gly	Asp	Met		
		130				135					140						
gtg	gtc	aag	gtc	tgg	gac	acc	agc	gct	gaa	agc	cgc	tac	ctg	gtg	ctg		480
Val	Val	Lys	Val	Trp	Asp	Thr	Ser	Ala	Glu	Ser	Arg	Tyr	Leu	Val	Leu		
145					150					155					160		
ccg	caa	cga	cca	gcg	ggc	tca	gag	cat	atg	agc	gaa	gag	cag	ttg	cgg		528
Pro	Gln	Arg	Pro	Ala	Gly	Ser	Glu	His	Met	Ser	Glu	Glu	Gln	Leu	Arg		
			165						170					175			
caa	ctg	gtc	acc	aag	gac	gtg	ctg	atc	ggc	gtc	gcc	ctg	ccc	cgc	gtt		576
Gln	Leu	Val	Thr	Lys	Asp	Val	Leu	Ile	Gly	Val	Ala	Leu	Pro	Arg	Val		
		180						185					190				
ggc	tga	gcaaggccgc	ccaaccccat	tcaacttccg	gagtggttcaa	t	atg	gat	ggc								632
Gly													Met	Asp	Gly		
														195			
ttt	cac	gat	ctc	ggc	ggt	ttc	cag	ggc	ttt	ggc	aaa	gtg	ccc	cac	cgc		680
Phe	His	Asp	Leu	Gly	Gly	Phe	Gln	Gly	Phe	Gly	Lys	Val	Pro	His	Arg		
			200					205					210				
atc	aac	agc	ctg	agc	tac	aag	cag	gtg	ttc	aag	cag	gac	tgg	gaa	cac		728
Ile	Asn	Ser	Leu	Ser	Tyr	Lys	Gln	Val	Phe	Lys	Gln	Asp	Trp	Glu	His		
		215					220					225					
ctg	gcc	tac	agc	ctg	atg	ttc	atc	ggc	gtc	gac	cac	ctg	aac	aag	ttc		776
Leu	Ala	Tyr	Ser	Leu	Met	Phe	Ile	Gly	Val	Asp	His	Leu	Asn	Lys	Phe		
		230				235					240						
agc	gtc	gac	gaa	ata	cgt	cat	gcc	gtc	gaa	cgc	att	gac	gtg	cgc	cag		824
Ser	Val	Asp	Glu	Ile	Arg	His	Ala	Val	Glu	Arg	Ile	Asp	Val	Arg	Gln		
245					250					255					260		
cac	gtc	ggc	acc	gaa	tac	tac	gaa	cgt	tat	gtg	atc	gcc	act	gcc	acg		872
His	Val	Gly	Thr	Glu	Tyr	Tyr	Glu	Arg	Tyr	Val	Ile	Ala	Thr	Ala	Thr		
			265					270						275			
ctg	ctg	gtc	gaa	aca	ggc	gtc	atc	acc	cag	gcc	gaa	ctg	gat	gaa	gca		920
Leu	Leu	Val	Glu	Thr	Gly	Val	Ile	Thr	Gln	Ala	Glu	Leu	Asp	Glu	Ala		
		280						285					290				
ctc	ggc	tcg	cac	ttc	aag	ctg	gcc	aac	ccc	gcc	cat	gcg	caa	ggg	cgt		968
Leu	Gly	Ser	His	Phe	Lys	Leu	Ala	Asn	Pro	Ala	His	Ala	Gln	Gly	Arg		
		295					300					305					
gct	gca	att	atc	ggg	cga	gcg	cct	ttt	gaa	gtg	ggc	gat	cgg	gtc	atc		1016
Ala	Ala	Ile	Ile	Gly	Arg	Ala	Pro	Phe	Glu	Val	Gly	Asp	Arg	Val	Ile		
		310				315					320						
gta	cgc	gat	gaa	tac	gtg	gcc	ggg	cat	gtg	cgc	atg	cct	gca	tac	gtg		1064
Val	Arg	Asp	Glu	Tyr	Val	Ala	Gly	His	Val	Arg	Met	Pro	Ala	Tyr	Val		

325	330	335	340	
cgc ggc aag caa ggc gta gtg ctg cac cgg acc act gaa cag tgg ccg				1112
Arg Gly Lys Gln Gly Val Val Leu His Arg Thr Thr Glu Gln Trp Pro	345	350	355	
ttt ccg gac gcg att ggc cat ggc gac cag agc gct gcg cat caa ccg				1160
Phe Pro Asp Ala Ile Gly His Gly Asp Gln Ser Ala Ala His Gln Pro	360	365	370	
acc tac cat gtc gag ttc cgc gtg cgg gac ctg tgg ggc gat gcc gca				1208
Thr Tyr His Val Glu Phe Arg Val Arg Asp Leu Trp Gly Asp Ala Ala	375	380	385	
gac gac ggc ctg gtg gtg gta gac ctg ttc gaa agc tat ctg gac agg				1256
Asp Asp Gly Leu Val Val Val Asp Leu Phe Glu Ser Tyr Leu Asp Arg	390	395	400	
gtc gaa agc ccg cga gtg gtg cgc gca tga gtgccggcgc ccaggcaggc				1306
Val Glu Ser Pro Arg Val Val Arg Ala	405	410		
cggtcgccgg tgacgggtcct ttcaggcttc ctccggcgag gcaagaccac cctgctcaac				1366
cacatcctgc gcaaccgccca gggcctgaag gtggcggtta tcgtcaatga catgagcgag				1426
gtcaacatcg atgccgccca ggtccagcgc gacgttgccg tgtatcgtgg ccaggatgaa				1486
ttgatagaga tgagcaacgg ctgtatctgc tgcaccctgc gcgccgacct gcttgagcag				1546
atcagcgcgc tggcgcgcca gcagcgtttc gattacctgt tgatcgagtc caccgggatt				1606
tccgagccga tgccagtcgc cgagaccttt gcctttctcg acgccaacgg tttcagcctc				1666
agcgaactgg cgcggctgga tacgctggtg acggtggtcg atgccagcca gttcatggcc				1726
atgctcgact ctcccgaac cgtcgcgcgg gccgacgtca ccacggatga cagcaggcgc				1786
ccgctggccg atctgctgat cgagcaggtc gagtatgccca atgtgattct ggtcaacaaa				1846
cgcgacctgg tcgacgaggc gcagtaccag gccctgcagg cagttctcgc cgggctcaat				1906
ccaggcgcac agatcctgcc gatggtggcc ggcaacgtcg ccctgtcgag cgtccttggt				1966
accagctgt tcgatttgcc cagccttgcc gcagcgcccg gctggatgaa acagatggac				2026
gcgcacgaca ccccgccgg cgagtcgcag acctatggcg tgacgtcatg ggtgtaccga				2086
gcgcgcgccc cgttccatcc gcaacgcttg cttgattttc tcgcccggcc ctggcgcgac				2146
ggccgtcttc tgcgcagcaa aggttatttc tggttgcca gccgccaccg cgaaatcggc				2206
ttgctggtac acagcggcca gcagtttcaa tgggactatg ttggccattg gtggaacttc				2266
atcgacacgt cacagtggcc acaggacaag tatcgcttgc agggcatcat ggccaagtgg				2326
gacagcatcg tcggcgactg ccgacaggag ctgaaaagct tatga				2371

<210> 7
<211> 193
<212> PRT
<213> Pseudomonas putida

<400> 7

Met Thr Ala Thr Ser Thr Pro Gly Glu Arg Ala Arg Ala Leu Phe Ala
1 5 10 15

Val Leu Lys Arg Lys Asp Leu Ile Pro Glu Gly Tyr Ile Glu Gln Leu
20 25 30

Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg Ile
35 40 45

Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Glu Leu Leu Leu Lys
50 55 60

Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Phe Thr Gly Pro Gln Gly
65 70 75 80

Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Gln Leu Lys Asn Val Ile
85 90 95

Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu Pro
100 105 110

Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg Glu
115 120 125

Gly Arg Thr Val Leu Arg Glu Leu Gly Thr Glu Leu Pro Gly Asp Met
130 135 140

Val Val Lys Val Trp Asp Thr Ser Ala Glu Ser Arg Tyr Leu Val Leu
145 150 155 160

Pro Gln Arg Pro Ala Gly Ser Glu His Met Ser Glu Glu Gln Leu Arg
165 170 175

Gln Leu Val Thr Lys Asp Val Leu Ile Gly Val Ala Leu Pro Arg Val
180 185 190

Gly

<210> 8
<211> 220

<212> PRT

<213> Pseudomonas putida

<400> 8

Met Asp Gly Phe His Asp Leu Gly Gly Phe Gln Gly Phe Gly Lys Val
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Pro His Arg Ile Asn Ser Leu Ser Tyr Lys Gln Val Phe Lys Gln Asp
20 25 30

Trp Glu His Leu Ala Tyr Ser Leu Met Phe Ile Gly Val Asp His Leu
35 40 45

Asn Lys Phe Ser Val Asp Glu Ile Arg His Ala Val Glu Arg Ile Asp
50 55 60

Val Arg Gln His Val Gly Thr Glu Tyr Tyr Glu Arg Tyr Val Ile Ala
65 70 75 80

Thr Ala Thr Leu Leu Val Glu Thr Gly Val Ile Thr Gln Ala Glu Leu
85 90 95

Asp Glu Ala Leu Gly Ser His Phe Lys Leu Ala Asn Pro Ala His Ala
100 105 110

Gln Gly Arg Ala Ala Ile Ile Gly Arg Ala Pro Phe Glu Val Gly Asp
115 120 125

Arg Val Ile Val Arg Asp Glu Tyr Val Ala Gly His Val Arg Met Pro
130 135 140

Ala Tyr Val Arg Gly Lys Gln Gly Val Val Leu His Arg Thr Thr Glu
145 150 155 160

Gln Trp Pro Phe Pro Asp Ala Ile Gly His Gly Asp Gln Ser Ala Ala
165 170 175

His Gln Pro Thr Tyr His Val Glu Phe Arg Val Arg Asp Leu Trp Gly
180 185 190

Asp Ala Ala Asp Asp Gly Leu Val Val Val Asp Leu Phe Glu Ser Tyr
195 200 205

Leu Asp Arg Val Glu Ser Pro Arg Val Val Arg Ala
210 215 220

<210> 9
 <211> 1089
 <212> DNA
 <213> Pseudomonas putida

<220>
 <221> CDS
 <222> (1)..(1089)
 <223> Coding region of activator protein gene

<400> 9
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 ggc ttc ctc ggc gca ggc aag acc acc ctg ctc aac cac atc ctg cgc 96
 Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg
 20 25 30
 aac cgc cag ggc ctg aag gtg gcg gtt atc gtc aat gac atg agc gag 144
 Asn Arg Gln Gly Leu Lys Val Ala Val Ile Val Asn Asp Met Ser Glu
 35 40 45
 gtc aac atc gat gcc gcc cag gtc cag cgc gac gtt gcg ctg tat cgt 192
 Val Asn Ile Asp Ala Ala Gln Val Gln Arg Asp Val Ala Leu Tyr Arg
 50 55 60
 ggc cag gat gaa ttg ata gag atg agc aac ggc tgt atc tgc tgc acc 240
 Gly Gln Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
 65 70 75 80
 ctg cgc gcc gac ctg ctt gag cag atc agc gcg ctg gcg cgc cag cag 288
 Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Ala Leu Ala Arg Gln Gln
 85 90 95
 cgt ttc gat tac ctg ttg atc gag tcc acc ggg att tcc gag ccg atg 336
 Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
 100 105 110
 cca gtc gcc gag acc ttt gcc ttt ctc gac gcc aac ggt ttc agc ctc 384
 Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asn Gly Phe Ser Leu
 115 120 125
 agc gaa ctg gcg cgg ctg gat acg ctg gtg acg gtg gtc gat gcc agc 432
 Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Ala Ser
 130 135 140
 cag ttc atg gcc atg ctc gac tct ccc gaa acc gtc gcg cgg gcc gac 480
 Gln Phe Met Ala Met Leu Asp Ser Pro Glu Thr Val Ala Arg Ala Asp
 145 150 155 160
 gtc acc acg gat gac agc agg cgc ccg ctg gcc gat ctg ctg atc gag 528
 Val Thr Thr Asp Asp Ser Arg Arg Pro Leu Ala Asp Leu Leu Ile Glu
 165 170 175
 cag gtc gag tat gcc aat gtg att ctg gtc aac aaa cgc gac ctg gtc 576
 Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Arg Asp Leu Val
 180 185 190

gac gag gcg cag tac cag gcc ctg cag gca gtt ctc gcc ggg ctc aat	624
Asp Glu Ala Gln Tyr Gln Ala Leu Gln Ala Val Leu Ala Gly Leu Asn	
195 200 205	
cca ggc gca cag atc ctg ccg atg gtg gcc ggc aac gtc gcc ctg tcg	672
Pro Gly Ala Gln Ile Leu Pro Met Val Ala Gly Asn Val Ala Leu Ser	
210 215 220	
agc gtc ctt ggt acc cag ctg ttc gat ttg ccc agc ctt gcc gca gcg	720
Ser Val Leu Gly Thr Gln Leu Phe Asp Leu Pro Ser Leu Ala Ala Ala	
225 230 235 240	
ccc ggc tgg atg aaa cag atg gac gcg cac gac acc ccg gcc ggc gag	768
Pro Gly Trp Met Lys Gln Met Asp Ala His Asp Thr Pro Ala Gly Glu	
245 250 255	
tcg cag acc tat ggc gtg acg tca tgg gtg tac cga gcg cgc gcc ccg	816
Ser Gln Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Ala Arg Ala Pro	
260 265 270	
ttc cat ccg caa cgc ttg ctt gat ttt ctc gcc cgg ccc tgg cgc gac	864
Phe His Pro Gln Arg Leu Leu Asp Phe Leu Ala Arg Pro Trp Arg Asp	
275 280 285	
ggc cgt ctt ctg cgc agc aaa ggt tat ttc tgg ctt gcc agc cgc cac	912
Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His	
290 295 300	
cgc gaa atc ggc ttg ctg gta cac agc ggc cag cag ttt caa tgg gac	960
Arg Glu Ile Gly Leu Leu Val His Ser Gly Gln Gln Phe Gln Trp Asp	
305 310 315 320	
tat gtt ggc cat tgg tgg aac ttc atc gac acg tca cag tgg cca cag	1008
Tyr Val Gly His Trp Trp Asn Phe Ile Asp Thr Ser Gln Trp Pro Gln	
325 330 335	
gac aag tat cgc ttg cag ggc atc atg gcc aag tgg gac agc atc gtc	1056
Asp Lys Tyr Arg Leu Gln Gly Ile Met Ala Lys Trp Asp Ser Ile Val	
340 345 350	
ggc gac tgc cga cag gag ctg aaa agc tta tga	1089
Gly Asp Cys Arg Gln Glu Leu Lys Ser Leu	
355 360	

<210> 10
 <211> 362
 <212> PRT
 <213> Pseudomonas putida

<400> 10

Met Ser Ala Gly Ala Gln Ala Gly Arg Leu Pro Val Thr Val Leu Ser
1 5 10 15

Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg
20 25 30

Asn Arg Gln Gly Leu Lys Val Ala Val Ile Val Asn Asp Met Ser Glu

35	40	45																	
Val	Asn	Ile	Asp	Ala	Ala	Gln	Val	Gln	Arg	Asp	Val	Ala	Leu	Tyr	Arg				
50						55					60								
Gly	Gln	Asp	Glu	Leu	Ile	Glu	Met	Ser	Asn	Gly	Cys	Ile	Cys	Cys	Thr				
65					70					75					80				
Leu	Arg	Ala	Asp	Leu	Leu	Glu	Gln	Ile	Ser	Ala	Leu	Ala	Arg	Gln	Gln				
				85					90					95					
Arg	Phe	Asp	Tyr	Leu	Leu	Ile	Glu	Ser	Thr	Gly	Ile	Ser	Glu	Pro	Met				
			100					105					110						
Pro	Val	Ala	Glu	Thr	Phe	Ala	Phe	Leu	Asp	Ala	Asn	Gly	Phe	Ser	Leu				
		115						120				125							
Ser	Glu	Leu	Ala	Arg	Leu	Asp	Thr	Leu	Val	Thr	Val	Val	Asp	Ala	Ser				
	130					135					140								
Gln	Phe	Met	Ala	Met	Leu	Asp	Ser	Pro	Glu	Thr	Val	Ala	Arg	Ala	Asp				
145					150					155					160				
Val	Thr	Thr	Asp	Asp	Ser	Arg	Arg	Pro	Leu	Ala	Asp	Leu	Leu	Ile	Glu				
				165					170					175					
Gln	Val	Glu	Tyr	Ala	Asn	Val	Ile	Leu	Val	Asn	Lys	Arg	Asp	Leu	Val				
			180					185					190						
Asp	Glu	Ala	Gln	Tyr	Gln	Ala	Leu	Gln	Ala	Val	Leu	Ala	Gly	Leu	Asn				
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Pro	Gly	Ala	Gln	Ile	Leu	Pro	Met	Val	Ala	Gly	Asn	Val	Ala	Leu	Ser				
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Ser	Val	Leu	Gly	Thr	Gln	Leu	Phe	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Ala				
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Pro	Gly	Trp	Met	Lys	Gln	Met	Asp	Ala	His	Asp	Thr	Pro	Ala	Gly	Glu				
				245					250					255					
Ser	Gln	Thr	Tyr	Gly	Val	Thr	Ser	Trp	Val	Tyr	Arg	Ala	Arg	Ala	Pro				
			260					265					270						
Phe	His	Pro	Gln	Arg	Leu	Leu	Asp	Phe	Leu	Ala	Arg	Pro	Trp	Arg	Asp				
		275					280					285							

Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
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Arg Glu Ile Gly Leu Leu Val His Ser Gly Gln Gln Phe Gln Trp Asp
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Tyr Val Gly His Trp Trp Asn Phe Ile Asp Thr Ser Gln Trp Pro Gln
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